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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/769,579	01/30/2004	James W. Schumm	016026-9238	2176

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EXAMINER	
GOLDBERG, JEANINE ANNE	
ART UNIT	**PAPER NUMBER**
1634	

SHORTENED STATUTORY PERIOD OF RESPONSE	MAIL DATE	DELIVERY MODE
3 MONTHS	01/26/2007	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

If NO period for reply is specified above, the maximum statutory period will apply and will expire 6 MONTHS from the mailing date of this communication.

Office Action Summary	Application No.	Applicant(s)	
	10/769,579	SCHUMM ET AL.	
	Examiner	Art Unit	
	Jeanine A. Goldberg	1634	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *06 November 2006*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *21-24* is/are pending in the application.

4a) Of the above claim(s) *22 and 23* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *21 and 24* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date *11/06*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

1. This action is in response to the papers filed November 6, 2006 and October 24, 2006. Currently, claims 21-24 are pending. Claims 22-23 have been withdrawn as drawn to non-elected subject matter.

Election/Restrictions

2. Applicant's election without traverse of HUMCSF1PO; HUMTPOX and HUMVWFA31in the paper filed May 18, 2006 is acknowledged.

Claims 22-23 are withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected invention, there being no allowable generic or linking claim.

The requirement is still deemed proper and is therefore made FINAL.

Priority

3. This application claims priority to several US applications.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

4. This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

5. Claims 21, 24 are rejected under 35 U.S.C. 103(a) as being unpatentable over Caskey (5,364,759) in view of GenBank STR loci HUMTPOX, HUMVWFA31 and HUMCSF1PO and further in view of Fregeau (BioTechniques, Vol. 15, No. 1, pages 100-119, 1993) or Kimpton (PCR Methods and Applications, Vol. 3, pages 13-22, 1993) or Urquhart (Int. J. Leg. Med, Vol. 107, pages 13-20, August 1994).

Caskey discloses the claimed method that includes obtaining a DNA sample, amplifying STR sequences from the DNA sample, and evaluating the amplification products for identification (col. 7, lines 4-10). Caskey describes a preferred Caskey discloses the claimed method that includes obtaining a DNA sample, amplifying STR sequences from the DNA sample, and evaluating the amplification products for identification (col. 7, lines 4-10). Caskey teaches a definition of "multiplex polymerase chain reaction (mPCR)"(col. 6, lines 34-68). Further, Caskey teaches that mPCR includes a) primers composed of similar GC base compositions and lengths, b) longer extensions times up to 8 fold the normally utilized times and c) minimization of

the number of PCR cycles performed to achieve detection. Caskey teaches that mPCR reaction is optimized for each reaction (col. 6, lines 65-66). Caskey identifies STR loci by searching all human sequences in GenBank (Example 1, col. 8). Strategies to determine the sequences flanking STRs are disclosed in Example 3 (col. 10). Although Caskey teaches that in a reaction with HUMARA and HUMFABP alleles appear as widely spaced doublets such that adjacent alleles overlap, different label may be applied to the different loci to unambiguously identify the alleles (col. 18). Caskey teaches the primers of SEQ ID NO: 15, 16, 19, 20, 27, and 28 as primers for the amplification of HUMFABP, HUMPRTB, and HUMTH01, respectively. As described in Example 7, the comparison of amplified alleles by polyacrylamide gel electrophoresis and visualization of the DNA by fluorescent analysis. STR markers can be detected with non-denaturing and denaturing electrophoretic systems. Silver staining detection methods are all applicable. Additionally, the loci are selected so that the amplification products of the alleles from different loci do not over lap. Further, Caskey teaches that the source of DNA to be tested can be any medial or forensic sample and can include blood, semen, vaginal swabs, tissue, hair, saliva, urine and mixtures of body fluids (col. 6, para. 2). Caskey discloses the use of allelic ladders as internal standards (col. 7, lines 15-19, and col. 19, lines 15-18). Additionally, Caskey teaches kits which contains a container having oligonucleotide primer pair for amplifying STRs and optionally, standards (col. 8 and col. 21, Example 10). Rather, than citing STR containing loci, Caskey refers to STR sequences by their alphabetical designation as indicated in Table I. Additionally, Caskey does not recite locus combinations in examples 4-7 and tables

6-9, where data from multiplex amplification of said alleles is performed and analyzed. Caskey describes the level of skill of an ordinary artisan by stating that once STR sequences and their flanking sequences are obtained, primer pairs may be designed and synthesized according to the flanking sequences and PCR amplification and comparison of amplified products may be performed to detect the short tandem repeats (col. 4, lines 9-17, col. 5, lines 16-53, col. 6, lines 58-60). Identical primers were used in the instant application for HUMFABP, HUMTH01, and HUMPRTB. Therefore, the method by which Caskey derives primers for STR loci appears to be consistent with the method of the instant application. Caskey also comments on the empirical nature of multiplex amplification reactions and points out that each reaction must be optimized (col. 6, line 65).

Caskey does not specifically teach the recited locus combinations.

However, the STR loci HUMTPOX, HUMVWFA31 HUMTH01 and HUMCSF1PO have been taught by GenBank Accession No: M68651, M25858, D00269 and X14720.

Fregeau teaches DNA typing with fluorescently tagged STRs for a sensitive and accurate approach to human identification. Fregeau teaches a multiplex system which contains HUMCD4, HUMFABP, and HUMCATBP2 (pg. 114, col. 3)(limitations of Claim 21, 48-54). DNA for the multiplex was extracted from blood, hair roots, dried bloodstains (pg. 101, col. 3, para. 1). Fregeau demonstrates that primers for STR systems HUMHPRT, HUMTH01, HUARA, HUMCD4, HUMFABP, HUMPLA2A1 and HUMRENA4 were used to amplify genomic DNA (pg. 102, col. 1, and Table 1). Fregeau teaches primers identical to the primers of SEQ ID NO: 1, 2, 9, 15, 16, 19, 20, 27, 28, and 30

(Table 1). Fregeau teaches HUMvWF, HumFABP, HumACTBP2 and D21S11 all have the same annealing temperature of 64 to 65 degrees and have shown to permit multiplex amplification which saves in reagents and sample template (pg. 117, col. 3, para 2). Further, HumCD4, HumARA, HumTHO01 have the same optimal annealing temperature, 68 degrees. The STR alleles were then separated and detected on a denaturing polyacrlamide gel electrophoresis (pg. 106). The fluorescent amplification products were resolved on polyacrylamide gels with various gel parameters varied (pg. 103, col. 1). A comparison was made between allele sized from silver-stained polyacrylamide gels and automated fluorescent analysis (pg. 110, col. 3). A four STR system, HUMCD4, HUMHPRT, HUMTH01, HumARA, was explored using additional amplification cycles. Fregeau describes multiplex amplification of polymorphic STR sequences of loci including HUMHPRTB, HUMTH01, HUMCD4, HUMFABP and HUMPLA2A (pg. 117, col. 3, para. 2). Empirical evaluation, a specific annealing temperature for each of the STR systems was found to generate consistent allelic profiles with high specificity and sensitivity after 28 cycles of amplification (pg. 115, col. 1). Several benefits of STRs analysis was elucidated including minimal only amounts of template DNA need to be used, the STR alleles can be resolved on sequencing gels using radiolabeled primers or having been processed with cold primers and detected after silver staining, and STRs are amenable to automation (pg. 100-101). Further, Fregeau teaches that careful selection of a refined polyacrylamide gel system and appropriate STR loci that have allele size ranges that are mutually resolvable should allow for additional systems to be analyzed with the same fluorescent tag (pg. 117, col.

3). Fregeau specifically teaches that multiplex amplification represents a savings in reagents and sample template.

Kimpton describes the multiplex amplification of polymorphic STR sequences of loci including HUMVWA31, HUMTH01, HUMF13A1, HUMFESFPS, HUMCD4, HUMDHER, HUMCYARO3, HUMAPOAII, HUMPLA2A, HUMIIDA, HUMFABP, HUMGABGA, HUMACTBP2 and D21S11. In Kimpton the combinations of loci are not identical to the combinations claimed. However, Kimpton performs multiplex amplification of STR containing loci in combinations of two, three, four, and seven, chosen loci from HUMVWA31, HUMTH01, HUMF13A1, HUMFESFPS, HUMCD4, HUMDHER, HUMCYARO3, HUMAPOAII, HUMPLA2A, HUMIIDA, HUMFABP, HUMGABGA, HUMACTBP2 and D21S11. Kimpton teaches primers for the amplification of HUMACTBP2, HMAPOAII, HUMFABP, HUMTH01, HUMvWA31/A which are identical to the primers taught in the instant application, namely SEQ ID NO: 1, 4, 15, 27, and 32. Kimpton teaches the PCR component concentrations and cycling parameters were optimized for each loci individually. The STRs suitable for co-amplification (multiplexing) were then selected on the basis of similar optimal reaction conditions and compatible allele size ranges (pg. 16, col. 1). Efficient amplification of all loci in multiplex systems was achieved by the adjustment of annealing temperature and individual primer concentration (pg. 19, col. 3). Further, STR loci with overlapping allele size ranges were differentiated by use of different fluorescent dye labels (pg. 16, col. 1).

Urquhart teaches a method of simultaneously determining the alleles present in at least two STR loci. Urquhart teaches a method of preparing DNA from whole blood

and performing a PCR amplification using genomic DNA. Each of two primers for each locus were added to the mixture and PCR was performed. The PCR products were electrophoresed in agarose gels, purified and sequenced (pg. 14, col. 1-2). Urquhart teaches primers which are identical to SEQ ID NO: 10, 15, 27, and 32 (Table 1) that correspond to HUMVWFA31 and HUMTHO1. Urquhart also teaches primers which are very homologous to SEQ ID NO: 11, 16, 25, 26 and 31. The alleles were evaluated by separating sizing alleles with an allelic ladder (pg. 14, col. 1). Further, Urquhart teaches markers used in the quadruplex STR system were labeled fluorescently (pg. 13-14). The DNA obtained was prepared from blood (pg. 14, col. 1). The conditions for the reaction were optimized in respect to the different STR's incorporated into the reaction (pg. 14, col. 2). The primers used in the study were all derived from the published or GenBank sequences (pg. 14, col. 1). Although Urquhart does not specifically teach **all** of the recited combinations disclosed in the instant application, Urquhart, does teach the amplification of HUMVWFA31, HUMTH01, HUMF13A01, HUMFES/FPS, HUMCD4, HUMPLA2A1, HUMFOLP23, HUMCYAR04, HUMTFIIDA, HUMFABP, HUMGABRB15, and HUMD21S11 (pg. 14, col. 2). Urquhart teaches that the annealing temperature for HUMTH01, HUMCD4, HUMPLA2A1, HUMFOLP23, HUMCYAR04, HUMTFIIDA, HUMFAB, HUMGABRB15 and HUMD21S11 are all 60 degrees (pg. 14, col. 2).

Therefore, to one of ordinary skill in the art at the time the invention was made, it would have been **prima facie** obvious to use any number of primers, including SEQ ID NO: 1-32, among other possible sequences that could accomplish the same goal for the process of simultaneously amplifying specified loci which provide a different pattern and

thus a means of confirmation or subsequent analysis. SEQ ID NO:s 1-14, 17-18, 21-26, 29-32 are not specifically taught by Caskey as specific primers for the respective STR loci. The claimed primers, however, would have been obvious based on the teaching of Caskey about primer design and synthesis and the known sequences of the claimed loci, which were available from GenBank. Additionally, Caskey was able to perform multiplex amplification of HUMTH01 in combination with other loci, which reiterates the level of skill in the art. As admitted in the specification, "successful combinations are generated by trial and error (routine experimentation) of locus combinations and by adjustment of primer concentrations to identify an equilibrium in which all included loci may be amplified"(pg. 10, lines 10-13). Therefore, the claimed invention would have been obvious over Caskey in view of the GenBank entries.

Response to Arguments

The response traversed the rejection in the parent application. The response asserts that Caskey provides no teaching as to which loci could be amplified to produce results that could be evaluated in any meaningful way because of the overlapping alleles. This argument has been reviewed but is not convincing because Caskey provides methods for choosing primers for use in multiplex analysis. Further the specification, "successful combinations are generated by trial and error (routine experimentation) of locus combinations and by adjustment of primer concentrations to identify an equilibrium in which all included loci may be amplified"(pg. 10, lines 10-13).

The response asserts that the references indicate that the selection of STR loci that can be co-amplified is not a trivial matter, but rather one that would require a

considerable amount of experimentation. This argument has been reviewed but is not convincing because the standard for obvious is not absolute expectation of success, but rather reasonable expectation of success. Given the teachings of the references there is a reasonable expectation of success. While some routine experimentation and optimization may be required to determine the exact parameters which allow successful optimization of the assay, this routine optimization is not an indice of non-obviousness. As noted in *In re Aller*, 105 USPQ 233 at 235, "More particularly, where the general conditions of a claim are disclosed in the prior art, it is not inventive to discover the optimum or workable ranges by routine experimentation." Routine optimization is not considered inventive and no evidence has been presented that the probe selection performed was other than routine, that the products resulting from the optimization have any unexpected properties, or that the results should be considered unexpected in any way as compared to the closest prior art. It is noted that this is not an invitation to file a declaration after final. As provided by MPEP 716.01, "Evidence traversing rejections must be timely or seasonably filed to be entered and entitled to consideration. In re Rothermel, 276 F.2d 393, 125 USPQ 328 (CCPA 1960). Affidavits and declarations submitted under 37 CFR 1.132 and other evidence traversing rejections are considered timely if submitted:(1) prior to a final rejection...."

MPEP 716.01(c) makes clear that "The arguments of counsel cannot take the place of evidence in the record. In re Schulze , 346 F.2d 600, 602, 145 USPQ 716, 718 (CCPA 1965). Examples of attorney statements which are not evidence and which must be supported by an appropriate affidavit or declaration include statements regarding

unexpected results, commercial success, solution of a long - felt need, inoperability of the prior art, invention before the date of the reference, and allegations that the author(s) of the prior art derived the disclosed subject matter from the applicant." Here, the statements regarding the unexpected results must be supported by evidence, not argument.

Thus for the reasons above and those already of record, the rejection is maintained.

6. Claims 21, 24 are rejected under 35 U.S.C. 103(a) as being unpatentable over Schumm et al. (US Pat. 5,783,406, July 21, 1998) in view of Fregeau (BioTechniques, Vol. 15, No. 1, pages 100-119, 1993) or Kimpton (PCR Methods and Applications, Vol. 3, pages 13-22, 1993) or Urquhart (Int. J. Leg. Med, Vol. 107, pages 13-20, August 1994).

Schumm teaches an assay for detecting at least one short tandem repeat sequence from DNA at a specific locus using an allelic ladder containing at least two short tandem repeat sequences. Schumm teaches allelic ladders for evaluating short tandem repeat sequences at a specific locus wherein the locus is selected from the group consisting of: HUMCD4, HUMCSF1PO, HUMCYP19 (CYARP450), HUMF13A01, HUMF13B, HUMFESFPS, HUMLPL (LIPOL), HUMPLA2A1 (PLA-AZ), HUMTPOX and HUMVWFA31. Schumm further teaches a multiplex method for analyzing HUMCSF1PO, HUMFESFPS, and HUMTH01 simultaneously. Schumm further teaches primers applicable for each of the STR.

Schumm does not specifically teach a multiplex method for analyzing HUMTPOX, HUMCSF1PO and HUMVWFA31.

However, Fregeau teaches DNA typing with fluorescently tagged STRs for a sensitive and accurate approach to human identification. Fregeau teaches a multiplex system which contains HUMCD4, HUMFABP, and HUMCATBP2 (pg. 114, col. 3)(limitations of Claim 21, 48-54). DNA for the multiplex was extracted from blood, hair roots, dried bloodstains (pg. 101, col. 3, para. 1). Fregeau demonstrates that primers for STR systems HUMHPRT, HUMTH01, HUARA, HUMCD4, HUMFABP, HUMPLA2A1 and HUMRENA4 were used to amplify genomic DNA (pg. 102, col. 1, and Table 1). Fregeau teaches primers identical to the primers of SEQ ID NO: 1, 2, 9, 15, 16, 19, 20, 27, 28, and 30 (Table 1). Fregeau teaches HUMvWF, HumFABP, HumACTBP2 and D21S11 all have the same annealing temperature of 64 to 65 degrees and have shown to permit multiplex amplification which saves in reagents and sample template (pg. 117, col. 3, para 2). Further, HumCD4, HumARA, HumTHO01 have the same optimal annealing temperature, 68 degrees. The STR alleles were then separated and detected on a denaturing polyacrlamide gel electrophoresis (pg. 106). The fluorescent amplification products were resolved on polyacrylamide gels with various gel parameters varied (pg. 103, col. 1). A comparison was made between allele sized from silver-stained polyacrylamide gels and automated fluorescent analysis (pg. 110, col. 3). A four STR system, HUMCD4, HUMHPRT, HUMTH01, HumARA, was explored using additional amplification cycles. Fregeau describes multiplex amplification of polymorphic STR sequences of loci including HUMHPRTB, HUMTH01, HUMCD4,

HUMFABP and HUMPLA2A (pg. 117, col. 3, para. 2). Empirical evaluation, a specific annealing temperature for each of the STR systems was found to generate consistent allelic profiles with high specificity and sensitivity after 28 cycles of amplification (pg. 115, col. 1). Several benefits of STRs analysis was elucidated including minimal only amounts of template DNA need to be used, the STR alleles can be resolved on sequencing gels using radiolabeled primers or having been processed with cold primers and detected after silver staining, and STRs are amenable to automation (pg. 100-101). Further, Fregeau teaches that careful selection of a refined polyacrylamide gel system and appropriate STR loci that have allele size ranges that are mutually resolvable should allow for additional systems to be analyzed with the same fluorescent tag (pg. 117, col. 3).

Kimpton describes the multiplex amplification of polymorphic STR sequences of loci including HUMVWA31, HUMTH01, HUMF13A1, HUMFESFPS, HUMCD4, HUMDHER, HUMCYARO3, HUMAPOAII, HUMPLA2A, HUMIIDA, HUMFABP, HUMGABGA, HUMACTBP2 and D21S11. In Kimpton the combinations of loci are not identical to the combinations claimed. However, Kimpton performs multiplex amplification of STR containing loci in combinations of two, three, four, and seven, chosen loci from HUMVWA31, HUMTH01, HUMF13A1, HUMFESFPS, HUMCD4, HUMDHER, HUMCYARO3, HUMAPOAII, HUMPLA2A, HUMIIDA, HUMFABP, HUMGABGA, HUMACTBP2 and D21S11. Kimpton teaches primers for the amplification of HUMACTBP2, HMAPOAII, HUMFABP, HUMTH01, HUMvWA31/A which are identical to the primers taught in the instant application, namely SEQ ID NO: 1, 4, 15, 27, and 32.

Kimpton teaches the PCR component concentrations and cycling parameters were optimized for each loci individually. The STRs suitable for co-amplification (multiplexing) were then selected on the basis of similar optimal reaction conditions and compatible allele size ranges (pg. 16, col. 1). Efficient amplification of all loci in multiplex systems was achieved by the adjustment of annealing temperature and individual primer concentration (pg. 19, col. 3). Further, STR loci with overlapping allele size ranges were differentiated by use of different fluorescent dye labels (pg. 16, col. 1).

Urquhart teaches a method of simultaneously determining the alleles present in at least two STR loci. Urquhart teaches a method of preparing DNA from whole blood and performing a PCR amplification using genomic DNA. Each of two primers for each locus were added to the mixture and PCR was performed. The PCR products were electrophoresed in agarose gels, purified and sequenced (pg. 14, col. 1-2). Urquhart teaches primers which are identical to SEQ ID NO: 10, 15, 27, and 32 (Table 1). Urquhart also teaches primers which are very homologous to SEQ ID NO: 11, 16, 25, 26 and 31. The alleles were evaluated by separating sizing alleles with an allelic ladder (pg. 14, col. 1). Further, Urquhart teaches markers used in the quadruplex STR system were labeled fluorescently (pg. 13-14). The DNA obtained was prepared from blood (pg. 14, col. 1). The conditions for the reaction were optimized in respect to the different STR's incorporated into the reaction (pg. 14, col. 2). The primers used in the study were all derived from the published or GenBank sequences (pg. 14, col. 1). Although Urquhart does not specifically teach **all** of the recited combinations disclosed in the instant application, Urquhart, does teach the amplification of HUMVWFA31, HUMTH01,

HUMF13A01, HUMFES/FPS, HUMCD4, HUMPLA2A1, HUMFOLP23, HUMCYAR04, HUMTFIIDA, HUMFABP, HUMGABRB15, and HUMD21S11 (pg. 14, col. 2). Urquhart teaches that the annealing temperature for HUMTH01, HUMCD4, HUMPLA2A1, HUMFOLP23, HUMCYAR04, HUMTFIIDA, HUMFAB, HUMGABRB15 and HUMD21S11 are all 60 degrees (pg. 14, col. 2).

Therefore, it would have been **prima facie** obvious to one of ordinary skill in the art at the time the claimed invention was made to have modified the teachings of Schumm with the loci of Fregeau, Kimpton or Urquhart to obtain the claimed invention because the skilled artisan would have been motivated by the teachings of Fregeau, Kimpton, or Urquhart to choose any reasonable number of known STR containing loci, and use them in desired combinations for detection and analysis of polymorphisms in STR loc. Further, it would have been obvious to have chosen any number of known STR containing loci which can be co-amplified together including those suggested by Schumm and use them in desired combinations for detection and analysis of polymorphisms in STR loci, because such a co-amplification was in fact performed by Kimpton, Fregeau and Urquhart. Both Kimpton (Int. J. Leg. Med), Fregeau, Kimpton and Urquhart teach intricate details of multiplex PCR reactions, such as critical parameters for primer design, optimization of cycling conditions, and pros and cons of gel electrophoresis, and visualization techniques (silver stain vs. fluorescence). Both Kimpton and Fregeau references comment on the empirical nature of selecting primers and amplification conditions to achieve an appropriate multiplex amplification system. Kimpton teaches "STRs suitable for co-amplification were selected on the basis of

similar optimal reaction conditions and compatible allele size ranges" (pg. 16, col. 1, para 3). For example, Fregeau teaches, HUMTH01 and HUMCD4 both have annealing temperatures of 68 degrees, and have different allele size (bp) which do not overlap (Table 1 and Table 3). Similarly, ACTBP2 and HUMFABP both have annealing temperatures of 64 degrees and do not have overlapping allele sizes (Table 1 and Table 3). Therefore the at least two STR loci would contain clearly distinguishable STR allelic profiles (pg. 115, col. 3) and would have been obvious to combine the two STR loci to obtain the claimed invention. The choice of STR loci chosen to multiplex is dependent on what information is desired from the allele analysis. As exemplified in the art, gel analysis of several STR loci on the same gel saved time and reagents. One of ordinary skill in the art would have been motivated to design appropriate primers and optimize PCR conditions in order to co-amplify additional combinations of STR loci for the benefit of saving time, reagents and other supplies in the amplification process as taught by Fregeau (pg. 117). It is also evident from these references that the loci were chosen for their already demonstrated polymorphic properties and that implementation of multiplex amplification of combinations thereof was easily achieved by routine optimization of the well known PCR methodology adapted for multiplex purposes. As admitted in the specification, "successful combinations are generated by trial and error (routine experimentation) of locus combinations and by adjustment of primer concentrations to identify an equilibrium in which all included loci may be amplified"(pg. 10, lines 10-13). Thus, the claimed invention would have been obvious over Schumm in view of Fregeau, Kimpton or Urquhart. Schumm specifically provides

the primer pairs for each of the STR loci. The ordinary artisan would have been motivated to expand the assay to the other loci taught by Schumm to enable further analysis and distinguishment of alleles, as taught by Schumm.

Response to Arguments

The response traverses the rejection. The response asserts that the references indicate that the selection of STR loci that can be co-amplified is not a trivial matter, but rather one that would require a considerable amount of experimentation. This argument has been reviewed but is not convincing because the standard for obvious is not absolute expectation of success, but rather reasonable expectation of success. Given the teachings of the references there is a reasonable expectation of success. While some routine experimentation and optimization may be required to determine the exact parameters which allow successful optimization of the assay, this routine optimization is not an indice of non-obviousness. As noted in *In re Aller*, 105 USPQ 233 at 235, "More particularly, where the general conditions of a claim are disclosed in the prior art, it is not inventive to discover the optimum or workable ranges by routine experimentation." Routine optimization is not considered inventive and no evidence has been presented that the probe selection performed was other than routine, that the products resulting from the optimization have any unexpected properties, or that the results should be considered unexpected in any way as compared to the closest prior art. It is noted that this is not an invitation to file a declaration after final. As provided by MPEP 716.01, "Evidence traversing rejections must be timely or seasonably filed to be entered and entitled to consideration. In re Rothermel, 276 F.2d 393, 125 USPQ 328 (CCPA 1960).

Affidavits and declarations submitted under 37 CFR 1.132 and other evidence traversing rejections are considered timely if submitted:(1) prior to a final rejection...."

MPEP 716.01(c) makes clear that "The arguments of counsel cannot take the place of evidence in the record. In re Schulze , 346 F.2d 600, 602, 145 USPQ 716, 718 (CCPA 1965). Examples of attorney statements which are not evidence and which must be supported by an appropriate affidavit or declaration include statements regarding unexpected results, commercial success, solution of a long - felt need, inoperability of the prior art, invention before the date of the reference, and allegations that the author(s) of the prior art derived the disclosed subject matter from the applicant." Here, the statements regarding the inoperability of the prior art must be supported by evidence, not argument.

Thus for the reasons above and those already of record, the rejection is maintained.

Conclusion

7. No claims allowable over the art.

8. Any inquiry concerning this communication or earlier communications from the examiner should be directed to examiner Jeanine Goldberg whose telephone number is (571) 272-0743. The examiner can normally be reached Monday-Friday from 7:00 a.m. to 4:00 p.m.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ram Shukla, can be reached on (571) 272-0735.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should

you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

The Central Fax Number for official correspondence is (571) 273-8300.

Jeanine Goldberg
Primary Examiner
January 8, 2007